

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 : Search time 7317.37 Seconds

(Without alignments)
11410.644 Million cell updates/sec

Title: US-09-910-428-3

Perfect score: 2869

Sequence: 1 ctctagagacccctcttctctgctg.....aatctagagagctllagagctc 2869

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank

1: gb-ba:*

2: gb-ba:*

3: gb-ba:*

4: gb-ba:*

5: gb-ba:*

6: gb-ba:*

7: gb-ba:*

8: gb-ba:*

9: gb-ba:*

10: gb-ba:*

11: gb-ba:*

12: gb-ba:*

13: gb-ba:*

14: gb-ba:*

15: gb-ba:*

16: gb-ba:*

17: gb-ba:*

18: gb-ba:*

19: gb-ba:*

20: gb-ba:*

21: gb-ba:*

22: gb-ba:*

23: gb-ba:*

24: gb-ba:*

25: gb-ba:*

26: gb-ba:*

27: gb-ba:*

28: gb-ba:*

29: gb-ba:*

30: gb-ba:*

31: gb-ba:*

32: gb-ba:*

33: gb-ba:*

34: gb-ba:*

35: gb-ba:*

36: gb-ba:*

37: gb-ba:*

38: gb-ba:*

39: gb-ba:*

40: gb-ba:*

41: gb-ba:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2817	98.2	25688	BTU15731	BTU15731 Bos taurus
2	1128.6	39.3	174419	AC119060	AC119060 Bos taurus
3	1128.6	39.3	208327	AC119061	AC119061 Bos taurus
4	1112.8	38.8	149984	AC109789	AC109789 Bos taurus
5	1107.8	38.6	135794	AC109791	AC109791 Bos taurus
6	1106	38.5	188500	AC109790	AC109790 Bos taurus
7	1104.4	38.5	167968	AC109787	AC109787 Bos taurus
8	1096.2	38.2	154998	AC109787	AC109787 Bos taurus
9	1089.2	38.0	174419	AC119060	AC119060 Bos taurus
10	1077.2	37.5	178028	AC109914	AC109914 Bos taurus
11	1076	37.5	190076	AC108895	AC108895 Bos taurus
12	1075.4	37.3	151482	AC109795	AC109795 Bos taurus
13	1069	37.3	151482	AC109795	AC109795 Bos taurus
14	1062.8	37.0	183383	AC091252	AC091252 Bos taurus
15	1059.2	36.9	166277	AC109794	AC109794 Bos taurus
16	1056.2	36.8	188497	AC092410	AC092410 Bos taurus
17	1053.2	36.7	186071	AC126230	AC126230 Bos taurus
18	1041.2	36.3	203696	AC087860	AC087860 Bos taurus
19	1040.6	36.3	154921	AC109793	AC109793 Bos taurus
20	1039.2	36.2	150594	AC108889	AC108889 Bos taurus
21	1033	36.0	157115	AC129070	AC129070 Bos taurus
22	1028.4	35.8	173207	AC108887	AC108887 Bos taurus
23	1026.4	35.8	156512	AC109792	AC109792 Bos taurus
24	1018.6	35.5	227410	AC108892	AC108892 Bos taurus
25	1011.8	35.3	165933	AC109797	AC109797 Bos taurus
26	1003.8	35.0	2955	HOV10195	HOV10195 Bos taurus
27	1003.4	35.0	134662	AC109786	AC109786 Bos taurus
28	1003.4	35.0	141089	AC109915	AC109915 Bos taurus
29	989	34.5	134652	AC109786	AC109786 Bos taurus
30	988.8	34.5	12039	AC109915	AC109915 Bos taurus
31	972.6	33.9	144582	BTU25810	BTU25810 Bos taurus
32	972.6	33.9	144582	AC096686	AC096686 Bos taurus
33	970.4	33.8	214803	AC096407	AC096407 Bos taurus
34	961.4	33.5	147922	AC087992	AC087992 Bos taurus
35	958.4	33.4	108538	AC108893	AC108893 Bos taurus
36	956.4	33.3	12222	HOV10195	HOV10195 Bos taurus
37	945	32.9	183311	AC109788	AC109788 Bos taurus
38	943.2	32.9	175942	AC107065	AC107065 Bos taurus
39	943	32.9	175942	AC107065	AC107065 Bos taurus
40	927.4	32.2	188500	AC109795	AC109795 Bos taurus
41	921.5	32.1	233345	AC121481	AC121481 Bos taurus
42	916.2	31.9	166277	AC109794	AC109794 Bos taurus
43	914.4	31.9	188121	AC093394	AC093394 Bos taurus
44	914.4	31.9	188121	AC093394	AC093394 Bos taurus
45	914	31.9	196377	AC105306	AC105306 Bos taurus

ALIGNMENTS

RESULT 1

LOCUS BTU15731 25688 bp DNA linear MAR 04-SEP-2001

DEFINITION Bos taurus somatotropin receptor gene, exon 1 and liver-specific promoter region.

ACCESSION U15731

VERSION U15731.2 GI:13570031

KEYWORDS

SOURCE Bos taurus.

ORGANISM Bos taurus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bovidae.

REFERENCE

1 (bases 1 to 25688)

Heup, D., Lucy, M.C., Collier, R.J., Boyd, C.K. and Warren, W.C.

Pred. No. is the number of results predicted by chance to have a

[illegible]

Assembly program	Fileset	Version	Q20 bases	Q40 bases
Consensus quality	155672		at least Q20	
Consensus quality	155215		bases at least Q40	
Consensus quality	155371		bases at least Q20	
Insert size	14000		aqarose-1p	
Insert size	157594		sum of cont.135	
Quality coverage	12.75X		in Q20 bases	aqarose-1p
Quality coverage	12.78X		in Q20 bases	sum of cont.135

NOTE: This is a working draft sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The first two contigs are believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

•	1	43557:	contig of 43557 bp in length
•	43558	44657:	gap of unknown length
•	44658	61202:	contig of 17545 bp in length
•	61203	61302:	gap of unknown length
•	61303	155794:	contig of 94492 bp in length.

Downloaded from www.sciencedirect.com

FEATURES
SOURCE
LOCATION/QUALIFIERS
1. 155794

Forgetting "Box Labels"
John, Eric - "Taxon: 9913"

misclassification 1.4357

vector side:left
1 22185

AC109790 clone RP42-60N24 (center project number).

misc: features 61303, .155794

Verfolgt nicht.

Address: "I have everything" with 2004gsk. A vaccination. Number
AC109789 clone 8042-399H12 (center project name 03g)
HATCH 030387 46625 3 20034 0 35648 g 50287 1 200 01415
ORIGIN

every Match	38.68;	Score 1107.8;	DB 2;	Length 155794;
at Local Similarity	93.34,	Fred. No. 2.56-256,		
Techns 1190;	Conservative	0;	Mismatches	82;
			Indels	3;
			Gaps	3;

[illegible]

1100 CTAAATATCTAAATTCAGTTTGGGACACGCTATACAGTGTCTCTCCGCACTTCCGAGCCCTCTCTC 1159

47110 CCAATATGAAATGCAATTCGGACAGGTATACATGCTTGGCATTCGTAACCCCTCTC 147169

1160 TTTCTTCTGATTAATTGGCTCTAGGACCGAAGCATGTCA 1218

1214 GCAATGACATACGAAACCTGCACTCCCAACCTCC - 1219
1220 GCGACACATGATATATTTACGATGCTGTCA 1227

47230 CTATCTTCATCAAACTTCAGCTGGCAACTTGTTCCTTACATGATATTACATGTTCA 147289

1 278 TTTTAACTTCGGAATTTTCATAAGCCTCATTAAGACTGTTC 1337

[illegible]

DB 147350 101AAGAGGAGGCTGCTTGGCTGGTCAATACCGGCTATGCTGCACTCTCTAAA 147409

[illegible]

1456 GATTAAGGCTCAGTTTAAACGCATTGAAGTCGATCAAGAATAAATGATGATTTTAA 1517

Db 147470 GATTAAAGCCTCCAGTTTCATCCAGCTCATTAAGAATGATTCGAATGATTCCTTTTAA 147529

[illegible]

1578 ATGACACATCAGGTTGCTTTCGATGTCCTGGCTATTATTAACACATGCTCTTCGATGAACATTG 1637

Lib 147530 AAGAAATCTAAGTTCCTGCGATCAGTTGGTGTGTTATTAATAACAGTGTGCGATGCAGCATTTG 147649

[illegible]

1698 CTGGATCATAGGCGAGTCTCATTTCCAGTTTTCAGGAATCTCCAGTGTCTGATA 1757

Db 147710 CCGATCATAAGGAGTCTATTTCTAGTTTAAAGAAATCTCAAAAGTCTCCATA 147769

[illegible]

by 1618 CCCCCCAHHHATTAATTGTAACCTTTGGAGTCCAGCGAATCTCAGTGGTGTCGAAT 1877

147830 CTTTCATTATTCATTATTTCTAGACTTTTCTGATCGAGGCATTCTTCACTGGTGTCAAT 147889

18/6 00A0CJALBaboo-11ballioAliliciliallMlgAbis91GAs; AlucTT 1936
|||||

57 1937 TCGATGCTGTTGCTTACGCCATCTGATCTCTTCTTCTTGGAGAGAAATCTCTAATTTAACTTCCTTTTCCG 1946

U6 147950 1CAAGGTGTTAGCCATCTATATGCTCTCTTGGAGAAAGTCTATTAGTCTCTTGG 148009

[illegible]

09-2027 TITLTGAMHACIIGIIIGTGGGICCTICATITGTATTITTNNANNAIIOAAI 2116

Db 14879 TTTTGAAATATGTTTGTGGTATGTTATTTGGTATATTTTCTGCACTGGAA 148129

2117 (G)GCTGTTTAAAGCTGTTGAAAGGTTAACTGTTTAAAGGTTAACTTA 2176

2177 GGTGGATTGTTATTTGTTTATTTCATATTCGGAGTCACTCTCCGCA 3386

[illegible]

96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 10

68 2297 ГИТЕЧНОСТЕЦИТЕ 2311

Db 148310 TTTCTGCTTACGT 148324

RESULT 6

LOCUS	188500 bp	DNA	linear	HTG 25-JUL-2001
DEFINITION	AC109790			
DESCRIPTION	Ros 1 locus clone pR43-AONDA	WORKING DRAFT	SEQUENCE	5' ordered

ACCESSION	AC109790
VERSION	AC109790.2
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT
SOURCE	Bos taurus,

REFERENCE	AUTHORS
1 (bases 1 to 188500)	Akhler, N., Antsoellis, A.

TITLE	JOURNAL	REFERENCE	AUTHORS
NISC Comparative Sequences	Unpublished	2 (bases 1 to 188500)	Crook, E. D.

JOURNAL. Submitted (07 FEB 2002)
GROVEMENT CIRCLE, 2319
REFERENCE 3 (bases 1 to 188500)

JOURNAL Submitted (25 JUL 2002)
GroveMont Circle, Gait
COMMENT On Jul 25, 2002 this s

Submitted 25 JUL 2002 NIH Intramural Sequencing Center, 87
 Grovemont Circle, Gaithersburg, MD 20877, USA
 On Jul 25, 2002 this sequence version replaced gi:18581929.
 ----- genome center -----
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc_200@imgrl.nih.gov
 ----- Project Information -----
 Center project name: axl
 Center clone name: 040N24

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated contid and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones; overlaps with neighboring clones; alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies: the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequence vector: *Flashtail_vfa_100%* of reads
Chemistry: Dye terminator Big Dye, 100% of reads
Assembly program: *Phrap*, version 0.990319
Consensus quality: 187613 bases at least Q40
Consensus quality: 187846 bases at least Q30
Consensus quality: 188010 bases at least Q20
Insert size: 135600, 188010 bases at least Q20
Insert size: 188100; sum-of-configs
Quality coverage: 12.73% at Q20 bases; sum-of-configs
Quality coverage: 9.14% at Q20 bases; sum-of-configs

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and

FEATURES

*	the accession number will be preserved.
*	1 156410: contig of 156410 bp in length
*	156411 156510: gap of unknown length
*	156511 170993: contig of 14483 bp in length
*	170994 171093: gap of unknown length
*	171094 181495: contig of 10402 bp in length
*	181496 181595: gap of unknown length
*	181596 187318: contig of 5723 bp in length
*	187319 187418: gap of unknown length
*	187419 188500: contig of 1082 bp in length.

Location/Qualifiers

misc_feature

misc_feature

misc_feature

misc_feature

misc_features

0000-0001-9786-400X

BASF CONT	58730	a	3A877	c	37404	q	53089	t	400 others
ORIGIN									

Query Match	36.6%	Score 1106, len 4	length 105600;
Best local Similarity	92.8%	Pred. NO. 6.7e-256;	
Matches 1193;	Conservative	0;	Mismatches 90; Indels 3; Gaps 3;

09 1029 AATGTTAAATTTTTTTTTCTGCATTTATTTATTTAACTTACATMATG 1088

Qy 1389 TATTAGTTTCTCAAAATCTCAAAAGAAATCCGACACAGTATATCAATGTTCCCATCC 1148

DB 13/20 IATAGIITTCGMAATGAAATGAACCCGCACAGTATACATGTGGTTCCCATCT 13661

DB 13660 GAATTTTCTTTCTTTTTCATAATCTTGGTAATGAGACCCAACTC 13601

[illegible]

1267 CAATATTATTATTATTATTAAATTTTCTAGGCTGTGGTAAGAATAAAGTGA 1326

1327 TAAAGCTGTTTATATATGAGTGTCTT1132715121621ACGAGCGGGA1A1151AAC 1386

Db 13480 TAGACTGTTCTATACATCAGTGTCTTTTGTGTTGTTACACGGGCTTATTTGTTACG 13421

Ubb 13420 ATCTTCTAAATTCATATATATGCGTTAGTATACGTGATTTGATCTTTTCCTTCTGGCT 13361

NOTE: This is a working draft sequence. It currently consists of 1000 bases. The first half of the file is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1266.695.7 : .7

HASE COUNT	a	b	c	d	e
ORIGIN	45594	32581	32935	43688	200 others

Query Match	38.28;	Score 1096.2;	DB 2;	Length 154968;
Host Label Similarity	97.08;	Pred. No. 1.5e 253;		
Matches 1149;	Conservative	0;	Mismatches 34;	Indels 3;
				Gaps 3

[illegible][illegible]

Herfman, B., Blakeley, R. W., Bouffard, G. S., Brown, K., Hinkley, C.,
 Brooks, S., Dietrich, N. L., Grunite, S., Guo, A., Gupta, J.,
 Hashiguchi, P., Hansen, N., Ho, S.-L., Idol, J. R., Kallins, E., Latic, P.,
 Lee-Lin, S.-Q., Legaspi, R., Maduro, O. L., Maduro, V. B.,
 MacQuiles, E. H., Mastello, C., Maskeri, B., Mastrian, S. D.,
 McCloskey, J. C., McDowell, J. C., Pasitigian, C., Pearson, R.,
 Portnoy, M. E., Prasad, A., Schuler, M. G., Staniford, S., Thomas, J. W.,
 Thomas, P. J., Touchman, J. W., Tsurgou, C., Vogt, J. L., Walker, M. A.,
 Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 174419)
 Green, E. D.
 Direct Submission
 Submitted (24-APR-2002) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

COMMENT

Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc.zoo@nih.gov
 Project Information
 Center project name: dbv
 Center clone name: 309101

Summary Statistics

Sequencing vector: Plasmid; n/a: 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.930319
 Consensus quality: 172887 bases at least Q40
 Consensus quality: 173012 bases at least Q30
 Consensus quality: 173165 bases at least Q20
 Insert size: 146000, average: 146000
 Insert size: 174119; sum-of-coverage
 Quality coverage: 10.13x in Q20 bases; sum-of-coverage
 Quality coverage: 8.50x in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 7424: contig of 7424 bp in length
 * 7425 7524: gap of unknown length
 * 7525 51203: contig of 43679 bp in length
 * 51204 51303: gap of unknown length
 * 51304 103342: contig of 52039 bp in length
 * 103343 103442: gap of unknown length
 * 103443 174419: contig of 70977 bp in length.

FEATURES

source

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 /organism="Sus laurus"
 /db_xref="taxon:9913"
 /clone="RP42.30911"
 /clone_id="RP42"

misc_feature

1..7424
 /note="assembly_fragment"

misc_feature

clone_end:516
 vector_side:right*

misc_feature

7525..51203
 /note="assembly_fragment"

misc_feature

51304..103342
 /note="assembly_fragment"

misc_feature

clone_end:17
 vector_side:right*

misc_feature

103443..174419
 /note="assembly_fragment"

misc_feature

BASE COUNT 54243 a 33533 c 32461 g 53882 t 360 others

misc_feature

ORIGIN

Query Match

38.0%; Score 1089.2; DB 2; Length 174419;

Best Local Similarity: 95.54; Prod. No. 7.4e 252;
 Matches 1178; Conservative 0; Mismatches 93; Indels 3; Gaps 3;
 1033 TTTTAATTTTTTTTTTCTCCATTTTATTTTAACTTACATTAATTTATT 1092
 10334 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1092
 50357 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 50298
 1094 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1152
 50297 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 50238
 1153 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1211
 50237 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 50178
 1212 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1270
 50177 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 50118
 1271 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1330
 50117 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 50058
 1331 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1390
 50057 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 49998
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 Matches 1180; Conservative 0; Mismatches 100; Indels 4; Gaps 4;

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 ACT09795
 VERSION
 ACT09795.1 GI:18582006
 KEYWORDS
 HTG; HTGS; PHASE1; HTGS_DRAFT.
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 Bovidae; Bovinae; Bos.
 REFERENCES
 1 (bases 1 to 205140)
 Akhtar, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, H.,
 Blackley, R.W., Bouffard, G.G., Brown, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Grant, S., Guan, X., Gupta, J., Haidich, P.,
 Ho, S.-L., Idol, J.R., Karlus, E., Latif, P., Lee, L.H., S. Q.,
 LeGrand, R., Maduro, O.L., Maduro, V.B., Mastaglio, C., Masker, R.,
 Mastropasqua, S., McElroy, J.C., McDowell, J., Pearson, R., Prasad, A.,
 Sturgeon, C., Voigt, L., Walker, M.A., Webster, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H., and Green, E.D.
 NIST Comparative Sequencing Initiative
 TITLE
 JOURNAL
 REFERENCE
 2 (bases 1 to 205140)
 Green, E.D.
 AUTHORS
 Direct Submission

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RESULT 15
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DEFINITION
Accession
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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 AC109794.1
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 Bos taurus.
 Bos taurus.
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 1 (bases 1 to 166277)
 Akhtar, N., Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B.,
 Blakesley, R. W., Bouliard, G. G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Hashiguchi, P.,
 Ho, S.-L., Idol, J. R., Karlins, E., Latic, P., Lee-Hin, S.-O.,
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 Mestrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Prasad, A.,
 Siantirnop, S., Thomas, D. M., Thomas, P. J., Touchman, J. W.,
 Tsurebon, C., Vogt, J. E., Walker, M. A., Welteby, K. D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E. D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 166277)
 Green, E. D.
 Direct Submission
 Submitted (07-FEB-2002) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>

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Contact: nisc.mouse@nhri.nih.gov
----- Project Information -----
Center project name: cjh
Center clone name: 499J06
----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166045 bases at least Q40
Consensus quality: 166073 bases at least Q30
Insert size: 143000; agarose-gel
Insert size: 16177; sum-of contigs
Quality coverage: 12.6% in Q20 bases;
quality coverage: 10.8% in Q20 bases; sum of contigs
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* NOTE: This is a "working draft" sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and they will be placed in their proper
* arbitrary gaps between the contigs as represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 51717 51816: gap of unknown length
* 51817 166277: contig of 114461 bp in length.
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Best Local Similarity 89.6%; Pred. No. 1.2e 244;
Matches 1172; Conservative 0; Mismatches 133; Indels 3; Gaps 3;
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